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RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/006,557

DATE: 12/17/2001
TIME: 11:01:04

Input Set : A:\36739A.txt
Output Set: N:\CRF3\12172001\J006557.raw

3 <110> APPLICANT: King, George L.
4 Abrahamson, Susan
5 Pugsley, Michael
7 <120> TITLE OF INVENTION: Modulation of Pericyte Proliferation
9 <130> FILE REFERENCE: 27129/36739A
C--> 11 <140> CURRENT APPLICATION NUMBER: US/10/006,557
C--> 11 <141> CURRENT FILING DATE: 2001-12-03
11 <150> PRIOR APPLICATION NUMBER: 60/250,542
12 <151> PRIOR FILING DATE: 2000-12-01
14 <160> NUMBER OF SEQ ID NOS: 15
16 <170> SOFTWARE: PatentIn version 3.1
18 <210> SEQ ID NO: 1
19 <211> LENGTH: 1813
20 <212> TYPE: DNA
21 <213> ORGANISM: Homo sapiens
23 <220> FEATURE:
24 <221> NAME/KEY: CDS
25 <222> LOCATION: (31)..(1491)
26 <223> OTHER INFORMATION:
29 <220> FEATURE:
30 <221> NAME/KEY: mat_peptide
31 <222> LOCATION: (124)..(1491)
32 <223> OTHER INFORMATION:
35 <220> FEATURE:
36 <221> NAME/KEY: misc_feature
37 <223> OTHER INFORMATION: rBPI
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42 Met Arg Glu Asn Met Ala Arg Gly
43 -30 -25
45 cct tgc aac ggc ccg aga tgg gtg tcc ctg atg gtg ctc gtc gcc ata 102
46 Pro Cys Asn Ala Pro Arg Trp Val Ser Leu Met Val Leu Val Ala Ile
47 -20 -15 -10
49 ggc acc gcc gtg aca gcg gcc gtc aac cct ggc gtc gtg gtc agg atc 150
50 Gly Thr Ala Val Thr Ala Ala Val Asn Pro Gly Val Val Val Arg Ile
51 -5 -1 1 5
53 tcc cag aag ggc ctg gac tac gcc agc cag cag ggg acg gcc gct ctg 198
54 Ser Gln Lys Gly Leu Asp Tyr Ala Ser Gln Gln Gly Thr Ala Ala Leu
55 10 15 20 25
57 cag aag gag ctg aag agg atc aag att cct gac tac tca gac agc ttt 246
58 Gln Lys Glu Leu Lys Arg Ile Lys Ile Pro Asp Tyr Ser Asp Ser Phe
59 30 35 40
61 aag atc aag cat ctt ggg aag ggg cat tat agc ttc tac agc atg gac 294
62 Lys Ile Lys His Leu Gly Lys Gly His Tyr Ser Phe Tyr Ser Met Asp
63 45 50 55
65 atc cgt gaa ttc cag ctt ccc agt tcc cag ata agc atg gtg ccc aat 342
66 Ile Arg Glu Phe Gln Leu Pro Ser Ser Gln Ile Ser Met Val Pro Asn

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67	60	65	70	
69	gtg ggc ctt aag ttc tcc atc agc aac gcc aat atc aag atc agc ggg			390
70	Val Gly Leu Lys Phe Ser Ile Ser Asn Ala Asn Ile Lys Ile Ser Gly			
71	75	80	85	
73	aaa tgg aag gca caa aag aga ttc tta aaa atg agc ggc aat ttt gac			438
74	Lys Trp Lys Ala Gln Lys Arg Phe Leu Lys Met Ser Gly Asn Phe Asp			
75	90	95	100	105
77	ctg agc ata gaa ggc atg tcc att tcg gct gat ctg aag ctg ggc agt			486
78	Leu Ser Ile Glu Gly Met Ser Ile Ser Ala Asp Leu Lys Leu Gly Ser			
79	110	115	120	
81	aac ccc acg tca ggc aag ccc acc atc acc tgc tcc agc tgc agc agc			534
82	Asn Pro Thr Ser Gly Lys Pro Thr Ile Thr Cys Ser Ser Cys Ser Ser			
83	125	130	135	
85	cac atc aac agt gtc cac atc tca aag agc aaa gtc ggg tgg			582
86	His Ile Asn Ser Val His Val His Ile Ser Lys Ser Lys Val Gly Trp			
87	140	145	150	
89	ctg atc caa ctc ttc cac aaa aaa att gag tct gcg ctt cga aac aag			630
90	Leu Ile Gln Leu Phe His Lys Lys Ile Glu Ser Ala Leu Arg Asn Lys			
91	155	160	165	
93	atg aac agc cag gtc tgc gag aaa gtg acc aat tct gta tcc tcc aag			678
94	Met Asn Ser Gln Val Cys Glu Lys Val Thr Asn Ser Val Ser Ser Lys			
95	170	175	180	185
97	ctg cca tat ttc cag act ctg cca gta atg acc aaa ata gat tct			726
98	Leu Gln Pro Tyr Phe Gln Thr Leu Pro Val Met Thr Lys Ile Asp Ser			
99	190	195	200	
101	gtg gct gga atc aac tat ggt ctg gtg gca cct cca gca acc acc acg gct			774
102	Val Ala Gly Ile Asn Tyr Gly Leu Val Ala Pro Pro Ala Thr Thr Ala			
103	205	210	215	
105	gag acc ctg gat gta cag atg aag ggg gag ttt tac agt gag aac cac			822
106	Glu Thr Leu Asp Val Gln Met Lys Gly Glu Phe Tyr Ser Glu Asn His			
107	220	225	230	
109	cac aat cca cct ccc ttt gct cca cca gtg atg gag ttt ccc gct gcc			870
110	His Asn Pro Pro Phe Ala Pro Pro Val Met Glu Phe Pro Ala Ala			
111	235	240	245	
113	cat gac cgc atg gta tac ctg ggc ctc tca gac tac ttc ttc aac aca			918
114	His Asp Arg Met Val Tyr Leu Gly Leu Ser Asp Tyr Phe Phe Asn Thr			
115	250	255	260	265
117	gcc ggg ctt gta tac caa gag gct ggg gtc ttg aag atg acc ctt aga			966
118	Ala Gly Leu Val Tyr Gln Glu Ala Gly Val Leu Lys Met Thr Leu Arg			
119	270	275	280	
121	gat gac atg att cca aag gag tcc aaa ttt cga ctg aca acc aag ttc			1014
122	Asp Asp Met Ile Pro Lys Glu Ser Lys Phe Arg Leu Thr Thr Lys Phe			
123	285	290	295	
125	ttt gga acc ttc cta cct gag gtg gcc aag aag ttt ccc aac atg aag			1062
126	Phe Gly Thr Phe Leu Pro Glu Val Ala Lys Lys Phe Pro Asn Met Lys			
127	300	305	310	
129	ata cag atc cat gtc tca gcc tcc acc ccg cca cac ctg tct gtg cag			1110
130	Ile Gln Ile His Val Ser Ala Ser Thr Pro Pro His Leu Ser Val Gln			
131	315	320	325	

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133	ccc acc ggc ctt acc ttc tac cct gcc gtg gat gtc cag gcc ttt gcc	1158
134	Pro Thr Gly Leu Thr Phe Tyr Pro Ala Val Asp Val Gln Ala Phe Ala	
135	330 335 340 345	
137	gtc ctc ccc aac tcc tcc ctg gct tcc ctc ctg att ggc atg cac	1206
138	Val Leu Pro Asn Ser Ser Leu Ala Ser Leu Phe Leu Ile Gly Met His	
139	350 355 360	
141	aca act ggt tcc atg gag gtc agc gcc gag tcc aac agg ctt gtt gga	1254
142	Thr Thr Gly Ser Met Glu Val Ser Ala Glu Ser Asn Arg Leu Val Gly	
143	365 370 375	
145	gag ctc aag ctg gat agg ctc ctg gaa ctg aag cac tca aat att	1302
146	Glu Leu Lys Leu Asp Arg Leu Leu Glu Leu Lys His Ser Asn Ile	
147	380 385 390	
149	ggc ccc ttc ccg gtt gaa ttg ctg cag gat atc atg aac tac att gta	1350
150	Gly Pro Phe Pro Val Glu Leu Leu Gln Asp Ile Met Asn Tyr Ile Val	
151	395 400 405	
153	ccc att ctt gtg ctg ccc agg gtt aac gag aaa cta cag aaa ggc ttc	1398
154	Pro Ile Leu Val Leu Pro Arg Val Asn Glu Lys Leu Gln Lys Gly Phe	
155	410 415 420 425	
157	cct ctc ccg acg ccg gcc aga gtc cag ctc tac aac gta gtg ctt cag	1446
158	Pro Leu Pro Thr Pro Ala Arg Val Gln Leu Tyr Asn Val Val Leu Gln	
159	430 435 440	
161	cct cac cag aac ttc ctg ctg ggt gca gac gtt gtc tat aaa	1491
162	Pro His Gln Asn Phe Leu Leu Phe Gly Ala Asp Val Val Tyr Lys	
163	445 450 455	
165	tgaaggcacc aggggtgccg ggggctgtca gccgcacctg ttccctgatgg gctgtggggc	1551
167	accggctgcc tttccccagg gaatcctctc cagatctaa ccaagagccc cttgc当地	1611
169	tcttcgactc agattcagaa atgatctaaa cacgaggaaa cattattcat tggaaaatgt	1671
171	catggtgtgt attttaggaa ttatgagctt ctttcaaggg ctaaggctgc agagatattt	1731
173	cctccagggaa tcgtgtttca attgtAACCA agaaaatttcc atttgtgtt catgaaaaaa	1791
175	aacttctggg tttttcatg tg	1813
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180	<212> TYPE: PRT	
181	<213> ORGANISM: Homo sapiens	
183	<220> FEATURE:	
184	<221> NAME/KEY: misc_feature	
185	<223> OTHER INFORMATION: rBPI	
187	<400> SEQUENCE: 2	
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193	Ser Leu Met Val Leu Val Ala Ile Gly Thr Ala Val Thr Ala Ala Val	
194	-15 -10 -5 -1 1	
197	Asn Pro Gly Val Val Val Arg Ile Ser Gln Lys Gly Leu Asp Tyr Ala	
198	5 10 15	
201	Ser Gln Gln Gly Thr Ala Ala Leu Gln Lys Glu Leu Lys Arg Ile Lys	
202	20 25 30	
205	Ile Pro Asp Tyr Ser Asp Ser Phe Lys Ile Lys His Leu Gly Lys Gly	
206	35 40 45	
209	His Tyr Ser Phe Tyr Ser Met Asp Ile Arg Glu Phe Gln Leu Pro Ser	

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210	50	55	60	65
213	Ser Gln Ile Ser Met Val Pro Asn Val Gly Leu Lys Phe Ser Ile Ser			
214		70	75	80
217	Asn Ala Asn Ile Lys Ile Ser Gly Lys Trp Lys Ala Gln Lys Arg Phe			
218		85	90	95
221	Leu Lys Met Ser Gly Asn Phe Asp Leu Ser Ile Glu Gly Met Ser Ile			
222		100	105	110
225	Ser Ala Asp Leu Lys Leu Gly Ser Asn Pro Thr Ser Gly Lys Pro Thr			
226		115	120	125
229	Ile Thr Cys Ser Ser Cys Ser Ser His Ile Asn Ser Val His Val His			
230		130	135	140
233	Ile Ser Lys Ser Lys Val Gly Trp Leu Ile Gln Leu Phe His Lys Lys			
234		150	155	160
237	Ile Glu Ser Ala Leu Arg Asn Lys Met Asn Ser Gln Val Cys Glu Lys			
238		165	170	175
241	Val Thr Asn Ser Val Ser Ser Lys Leu Gln Pro Tyr Phe Gln Thr Leu			
242		180	185	190
245	Pro Val Met Thr Lys Ile Asp Ser Val Ala Gly Ile Asn Tyr Gly Leu			
246		195	200	205
249	Val Ala Pro Pro Ala Thr Thr Ala Glu Thr Leu Asp Val Gln Met Lys			
250		210	215	220
253	Gly Glu Phe Tyr Ser Glu Asn His His Asn Pro Pro Pro Phe Ala Pro			
254		230	235	240
257	Pro Val Met Glu Phe Pro Ala Ala His Asp Arg Met Val Tyr Leu Gly			
258		245	250	255
261	Leu Ser Asp Tyr Phe Phe Asn Thr Ala Gly Leu Val Tyr Gln Glu Ala			
262		260	265	270
265	Gly Val Leu Lys Met Thr Leu Arg Asp Asp Met Ile Pro Lys Glu Ser			
266		275	280	285
269	Lys Phe Arg Leu Thr Thr Lys Phe Phe Gly Thr Phe Leu Pro Glu Val			
270		290	295	300
273	305			
274	Ala Lys Lys Phe Pro Asn Met Lys Ile Gln Ile His Val Ser Ala Ser			
277		310	315	320
278	Thr Pro Pro His Leu Ser Val Gln Pro Thr Gly Leu Thr Phe Tyr Pro			
281		325	330	335
282	Ala Val Asp Val Gln Ala Phe Ala Val Leu Pro Asn Ser Ser Leu Ala			
285		340	345	350
286	Ser Leu Phe Leu Ile Gly Met His Thr Thr Gly Ser Met Glu Val Ser			
289		355	360	365
290	Ala Glu Ser Asn Arg Leu Val Gly Glu Leu Lys Leu Asp Arg Leu Leu			
293		370	375	380
294	Leu Glu Leu Lys His Ser Asn Ile Gly Pro Phe Pro Val Glu Leu Leu			
297		390	395	400
298	Gln Asp Ile Met Asn Tyr Ile Val Pro Ile Leu Val Leu Pro Arg Val			
301		405	410	415
302	Asn Glu Lys Leu Gln Lys Gly Phe Pro Leu Pro Thr Pro Ala Arg Val			
305		420	425	430
306	Gln Leu Tyr Asn Val Val Leu Gln Pro His Gln Asn Phe Leu Leu Phe			
	435	440	445	

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309 Gly Ala Asp Val Val Tyr Lys
310 450 455
313 <210> SEQ ID NO: 3
314 <211> LENGTH: 11
315 <212> TYPE: PRT
316 <213> ORGANISM: Homo sapiens
318 <220> FEATURE:
319 <221> NAME/KEY: MISC_FEATURE
320 <223> OTHER INFORMATION: XMP.679
323 <220> FEATURE:
324 <221> NAME/KEY: SITE
325 <222> LOCATION: (5)..(5)
326 <223> OTHER INFORMATION: /label=Substituted-Ala note=position 5 is 1- naph-ala
329 <220> FEATURE:
330 <221> NAME/KEY: SITE
331 <222> LOCATION: (9)..(9)
332 <223> OTHER INFORMATION: /label=Substituted-Ala note=position 9 is 1- naph-ala
335 <220> FEATURE:
336 <221> NAME/KEY: SITE
337 <222> LOCATION: (1)..(11)
338 <223> OTHER INFORMATION: /Label=D Amino Acids/note=Positions 1-11 are D-Amino Acids
341 <220> FEATURE:
342 <221> NAME/KEY: SITE
343 <222> LOCATION: (11)..(11)
344 <223> OTHER INFORMATION: AMIDATION /label=Amidation note=The C-terminus is Amidated
347 <400> SEQUENCE: 3
349 Lys Leu Phe Lys Ala Gln Ala Lys Ala Lys Gly
350 1 5.. 10
353 <210> SEQ ID NO: 4
354 <211> LENGTH: 11
355 <212> TYPE: PRT
356 <213> ORGANISM: Homo sapiens
358 <220> FEATURE:
359 <221> NAME/KEY: MISC_FEATURE
360 <223> OTHER INFORMATION: XMP.627
363 <220> FEATURE:
364 <221> NAME/KEY: SITE
365 <222> LOCATION: (5)..(5)
366 <223> OTHER INFORMATION: /label=Substituted Ala note=position 5 is 1-naph-ala
369 <220> FEATURE:
370 <221> NAME/KEY: SITE
371 <222> LOCATION: (9)..(9)
372 <223> OTHER INFORMATION: /label=Substituted Ala note=position 9 is 1- naph-ala
375 <220> FEATURE:
376 <221> NAME/KEY: SITE
377 <222> LOCATION: (1)..(11)
378 <223> OTHER INFORMATION: /Label=D Amino Acids/note=Positions 1-11 are D-amino acids
381 <220> FEATURE:
382 <221> NAME/KEY: SITE

VERIFICATION SUMMARY

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Input Set : A:\36739A.txt

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L:11 M:270 C: Current Application Number differs, Replaced Current Application No

L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date